

FIGURE 1

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGCCCCGCGCCCAG
TC**ATG**ACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGCTGCTCAGTGCGGCGGTGTGCCGGG
CTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCAT
GTGCCGAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTG
ACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGTC
TTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGGAAAACGGGGATTTC
CACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGC
TAAAGCTGGTGAAGGGCATTTCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATC
ACCTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAA
AGAAA**TAA**TAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGCCCCGCGCCCAG
TCATGACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGCTGCTCAGTGCGGCGGTGTGCCGGG
CTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCAT
GTGCCGAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTG
ACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGTC
TTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGGAAAACGGGGATTTC
CACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGC
TAAAGCTGGTGAAGGGCATTTCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATC
ACCTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAA
AGAAA**TAA**TAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

CGCGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCAGGGAGTGTCCCGGCTGGCCTAGG
CAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCTGCTCAGCTTCCTGGGCATGGTGGGCA
CGTTGATCACCAACCATCCTGCCGCACTGGCGGAGGACAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCT
ACCTGAAAGGGCTCTGGATGGAGTGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGC
TGGCGCTGCCCCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCG
CCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTGCCATCCTCG
GCGGCACCCCTCTTCATCCTGGCCGGCCCTCCTGTGCATGGTGGCCGTCTCCTGGACCACCAACGACGTGGTGCAGA
ACTTCTACAACCCGCTGCTGCCAGCGGCATGAAGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCT
CGTCCCTCTCGCTCATTGGTGGCACCCCTGCTTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGG
CCCCGCCCAGGGCCACCACGACCACTGCAAAACCCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATC
GGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG**TGA**GTCCTCCACAGCCTGCT
TCTCCCTTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGGTTCCAGCACAAAGTTTAC
TTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGG
AAATAAGAGGAGGAGAAAGCTCTCTATACCAAAAGACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATTATAT
ATATTTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGAAGTGGGAGTTTGGTCAGTGGGGTTGGTTTGTG
ATCCAGGAATAAACCTTGCGGATGTGGCTGTTTTATGAAAAAAAAAAAAA

FIGURE 3

CAGGACCAGGTCTTCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG
 ATCCTGCTGACGCTGGGCCCCGCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG
 GAGAAGCCACTGCCCACCGCTTCTTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCTGACTGGCTGAAGCTG
 CGCATGATCCGTTCTGAGGTGCTCCGCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTG
 TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCCTCCAGTTCTTGGACCAGGCAGTGGCCCCAC
 GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCCACCTGGTGGAGGTCCAGCATGAGCGC
 GGCGCTCCGGAGGCCAGACTTTCACCTCCTTGCTCACAGCCTCCCTGCCGCCCCGCCGAGACAGCACAGAGGCA
 CCCAAACCAAAGAGCAGCCAGAGCAGCCCATAGGCCAGGGCCGGATTTCGGGTGGGGACCCAGCTCCGGGTGCTG
 GGCCCTGAGGACGACCTGGCTGGCATGTTCTCCAGATTTTCCGCTCAGCCCCGACCCTCGGTGGCAGAGCTCC
 AGTCCCCGCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCCGCTCGTCCAGGGCAGCCCC
 GAGGTGCCGGGCATCACGGTGCCTGTCTGCAGGCCCTCGCCACCCTGCTCAGCTCCCCACACGGCGGTGCCCTG
 GTGATGTCCATGCACCGTAGCCACTTCTGGCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGTG
 CCACAGGACACCGGCTTCTCCTCGCTCTTCTGAAGGTGCTCCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC
 GTGGAGGGCGGGCCCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCCCTCAGCCGGGCGCAGGCTCAGTGAT
 GTGCGAGGGGGGCTCCTGCGCCTGGCCGAGGCCCTGGCCTTCCGTGAGGACCTGGAGGTGGTTCAGCTCCACCGTC
 CGTGCCGTGATCGCCACCCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGACCTGATCAGCAAAGTCTCCAG
 GGGCTGATCGAGGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTCTGCCACTGCGGATGCTGCC
 TCCCCGTTTCCAGCCTGTAAGCCCGTTGTGGTGGTGAAGTCCCTGCTGCTGCAGGAGGAGGAGCCCCCTGGCTGGG
 GGGAAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCTCGTCAGGCCCTCCTAGTGGACTGG
 CTGGAAATGCTGGACCCCGAGGTGGTCAGCAGCTGCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGAGGAAG
 GGCAAAGGTGAGGCCAGGTGCCCTCGTTCCGTCCCTACCTCCTGACCCTCTTACGCATCAGTCCAGCTGGCCC
 AACTGACACAGTGCATCCGAGTCTGCTGGGCAAGAGCCGGGAACAGAGGTTCCAGCCCTCTGCCTCTCTGGAC
 TTCTCTGGGCCTGCATCCATGTTCTCCTCGCATCTGGCAGGGGCGGGACCAGCGCACCCCGCAGAAGCGGCGGGAG
 GAGCTGGTGTGCGGGTCCAGGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG
 AGCCAGGACGGGGACACAGCCGCCCTGCAGCCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG
 GACGATGAGAGTGTGAGGAAGGTGACGGAGCACCTGTGAGGCTGCATCCAGCAGTGGGGAGACAGCGTGTGGGA
 AGGCGCTGCCGAGACCTTCTCCTGCAGCTCTACCTACAGCGGCCCGGAGCTGCGGGTGGCCGTGCTGAGGTCTTA
 CTGCACAGCGAAGGGGTGCCAGCAGCAGCGTCTGCAAGCTGGACGGACTCATCCACCGCTTCATCACGCTCCTT
 GCGGACACCAGCGACTCCCCGGGCGTTGGAGAACCAGGGGGCGGATGCCAGCATGGCCTGCCGGAAGCTGGCGGTG
 GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCCTGCACGGCCGCACCCACCTCAACTTC
 CAGGAGTTCCGGCAGCAGAACCACCTGAGCTGCTTCTGACAGTGTGCGGCTGCTGGAGTGTGCTGCAGCCGCAC
 GTGTTCCGCAGCAGCAGCAGGGGGCGCTGTGGGACTGCCTTCTGTCTTCATCCGCCTGCTGCTGAATTACAGG
 AAGTCTTCCCGCCATCTGGCTGCCTTCATCAACAAGTTTGTGCAGTTTCATCCATAAGTACATTACCTACAATGCC
 CCAGCAGCCATCTCCTTCTGAGAAAGCAGCCGACCCGCTCCACGACCTGTCTTCGACAACAGTGACCTGGTG
 ATGCTGAAATCCCTCCTTGCAGGGCTCAGCCTGCCAGCAGGGACGACAGGACCGACCGAGGCCTGGACGAAGAG
 GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGGCCCTGGTTCAGCGTCTCCTGTTACCCCTCTGACCGCGGCCGAG
 ATGGCCCCCTACATGAAACGGCTTTCGCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
 GAGATGTCCCGGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG
 GAGTGTGCGCAACCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTC
 CTGCCCACGTTTCATGTAAGTGCCTGGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTGAG
 TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGGCTTCTGGTGGGCATGTACGGCCAGATG
 GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGTGAGCCTGTGGCAGCCGA
 CCCCCCTCAAGCCCCGGCCCCGTCCCGTCCCCGGGGATCCTCGAGGCAAAGCCAGGAAGCGTGGGCGTTGCTGG
 TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGCAGGCCAGGAGCAATACTCCGAGCCCTGGGGTGG
 CTCCGGGCGGCGGCTGGCATCAGGGGCCGTCCAGCAAGCCCTCATTCACCTTCTGGGCCACAGCCCTGCCGCGG
 AGCGGCGGATCCCCCGGGCATGGCTGGGTGGTGGTGAATGAAACGACCTGAAGTGTCAA

FIGURE 5

MTLRPSLLPLHLLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHIHYTGSLVDGRIID
TSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGFPSPVPADAVVQYDVELIALIRANYWL
KLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVSKKKLKEEKRNSKKK

Signal peptide.

amino acids 1-25

Transmembrane domain.

amino acids 155-174

N-glycosylation site.

amino acids 196-200

N-myristoylation site.

amino acids 95-101

Amidation site.

amino acids 119-123

FKBP-type peptidyl-prolyl cis-trans isomerase signature 1.

amino acids 62-78, 87-124, 128-142

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FIGURE 6

MASTAVQLLGFLLSFLGMVGTLLTITLPHWRRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQCQIYRSLLALPQ
DLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTFAILGGTLFILAGLLCMVAVSWTTNDVVQNFYNP
LLPSGMKFEEIGQALYLGFISSSLIGGTLCLSCQDEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSV
TSATHSGYRLNDYV

Signal sequence.

amino acids 1-21

Transmembrane domains.

amino acids 78-98, 116-136, 162-182

N-myristoylation sites.

amino acids 17-22, 20-25, 60-65, 92-97, 101-106, 178-183

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 85-95, 87-97

PMP-22/EMP/MP20/Claudin family.

amino acids 4-181

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FIGURE 7

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRMIRSEVLRLVDAAL
 QDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNYMAHLVEVQHERGASGGQTFHSLLTAS
 LPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLGPEDDLQAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQ
 ELARVVQGSPEVPGITVRVLQALATLLSSPHGGALVMSMRSHFLACPLLRLCQYQRCVPQDTGFSSFLKVL
 QMLQWLDSPGVEGGPLRAQLRMLASQASAGRRLSDVRGGLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQCSV
 EPDLISKVLQGLIEVRSPLHEELLTAFFSATADAASFPACKPVVVSSLLLQEEEPLAGGKPGADGGSLEAVRL
 GPSSGLLDVWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFRPYLLTLFTHQSSWPTLHQCIRVLLGKSRE
 QRFDPASLDFLWACIHVPRIWQGRDQRTQPQRREELVLRVQGPSELISLVELILAEAETRSQDGDTAACSLIQAR
 LPLLLSCCCGDDSEVRKVTEHLSGCIQQWGDSVLGRRCRDLLLQLYLQRPVLPVPEVLLHSEGAASSSVCKLD
 GLIHRFITLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPMAALLHGRTHLNFQEFQQNHLSCFLHV
 LGLELLQPHVFRSEHQGALWDCLLSFIRLLLNYRKSSRHAAAFINKFVQFIHKYITYNAPAAISFLQKHADPLH
 DLSFDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAGSLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVE
 DLLEVLSDIDEMSRRRPEILSFFSTNLQRLMSSAECCRNLAFLSLALRSMQNSPSIAAFLPTFMVCLGSQDFEV
 VQTALRNLPYALLCQEHA AVLHRAFLVGMYGMDPSAQISEALRILHMEAVM

Signal peptide.

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449, 665-671,
 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 8

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF
SMPEVNVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSC
MIENDIAKATGDIKVTSEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYMLLK

Signal peptide.

amino acids 1-28

Transmembrane domain.

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220, 220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

Immunoglobulin domain.

amino acids 49-132

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